



2590  
0129

ENTERED

OIPE

## RAW SEQUENCE LISTING

DATE: 01/29/2003 *fb*

PATENT APPLICATION: US/09/983,025A

TIME: 13:54:04

Input Set : A:\sequence listing.txt

Output Set: N:\CRF4\01292003\I983025A.raw

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3 <110> APPLICANT: OXVIG, Claus
4   OVERGAARD, Michael T.
6 <120> TITLE OF INVENTION: PREGNANCY-ASSOCIATED PLASMA PROTEIN-A2 (PAPP-A2)
8 <130> FILE REFERENCE: OXVIG=1A
10 <140> CURRENT APPLICATION NUMBER: US 09/983,025A
11 <141> CURRENT FILING DATE: 2001-10-22
13 <150> PRIOR APPLICATION NUMBER: US 60/241,840
14 <151> PRIOR FILING DATE: 2000-10-20
16 <150> PRIOR APPLICATION NUMBER: DK PA 2000 01571
17 <151> PRIOR FILING DATE: 2000-10-20
19 <160> NUMBER OF SEQ ID NOS: 26
21 <170> SOFTWARE: PatentIn version 3.2
23 <210> SEQ ID NO: 1
24 <211> LENGTH: 8527
25 <212> TYPE: DNA
26 <213> ORGANISM: Homo sapiens
29 <220> FEATURE:
30 <221> NAME/KEY: CDS
31 <222> LOCATION: (1)..(5373)
32 <223> OTHER INFORMATION: prepro-PAPP-A2 coding sequence
34 <220> FEATURE:
35 <221> NAME/KEY: sig_peptide
36 <222> LOCATION: (1)..(66)
38 <220> FEATURE:
39 <221> NAME/KEY: misc_feature
40 <222> LOCATION: (1)..(66)
41 <223> OTHER INFORMATION: prepro part of PAPP-A2
43 <220> FEATURE:
44 <221> NAME/KEY: misc_feature
45 <222> LOCATION: (67)..(699)
46 <223> OTHER INFORMATION: pro part of PAPP-A2
48 <220> FEATURE:
49 <221> NAME/KEY: mat_peptide
50 <222> LOCATION: (700)..()
52 <220> FEATURE:
53 <221> NAME/KEY: 3'UTR
54 <222> LOCATION: (5377)..(8527)
56 <400> SEQUENCE: 1
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58 Met Met Cys Leu  Lys Ile Leu Arg Ile  Ser Leu Ala Ile Leu  Ala
59          -230          -225          -220
61 ggg tgg gca ctc  tgt tct gcc aac tct  gag ctg ggc tgg aca  cgc      90
62 Gly Trp Ala Leu  Cys Ser Ala Asn Ser  Glu Leu Gly Trp Thr  Arg

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63	-215	-210	-205	
65	aag aaa tcc ttg gtt gag agg gaa cac ctg aat cag gtg ctg ttg	135		
66	Lys Lys Ser Leu Val Glu Arg Glu His Leu Asn Gln Val Leu Leu			
67	-200	-195	-190	
69	gaa gga gaa cgt tgt tgg ctg ggg gcc aag gtt cga aga ccc aga	180		
70	Glu Gly Glu Arg Cys Trp Leu Gly Ala Lys Val Arg Arg Pro Arg			
71	-185	-180	-175	
73	gct tct cca cag cat cac ctc ttt gga gtc tac ccc agc agg gct	225		
74	Ala Ser Pro Gln His His Leu Phe Gly Val Tyr Pro Ser Arg Ala			
75	-170	-165	-160	
77	ggg aac tac cta agg ccc tac ccc gtg ggg gag caa gaa atc cat	270		
78	Gly Asn Tyr Leu Arg Pro Tyr Pro Val Gly Glu Gln Glu Ile His			
79	-155	-150	-145	
81	cat aca gga cgc agc aaa cca gac act gaa gga aat gct gtg agc	315		
82	His Thr Gly Arg Ser Lys Pro Asp Thr Glu Gly Asn Ala Val Ser			
83	-140	-135	-130	
85	ctt gtt ccc cca gac ctg act gaa aat cca gca gga ctg agg ggt	360		
86	Leu Val Pro Pro Asp Leu Thr Glu Asn Pro Ala Gly Leu Arg Gly			
87	-125	-120	-115	
89	gca gtt gaa gag ccg gct gcc cca tgg gta ggg gat agt cct att	405		
90	Ala Val Glu Glu Pro Ala Ala Pro Trp Val Gly Asp Ser Pro Ile			
91	-110	-105	-100	
93	ggg caa tct gag ctg ctg gga gat gat gac gct tat ctc ggc aat caa	453		
94	Gly Gln Ser Glu Leu Leu Gly Asp Asp Asp Ala Tyr Leu Gly Asn Gln			
95	-95	-90	-85	
97	aga tcc aag gag tct cta ggt gag gcc ggg att cag aaa ggc tca gcc	501		
98	Arg Ser Lys Glu Ser Leu Gly Glu Ala Gly Ile Gln Lys Gly Ser Ala			
99	-80	-75	-70	
101	atg gct gcc act act acc acc gcc att ttc aca acc ctg aac gaa ccc	549		
102	Met Ala Ala Thr Thr Thr Thr Ala Ile Phe Thr Thr Leu Asn Glu Pro			
103	-65	-60	-55	
105	aaa cca gag acc caa agg agg ggc tgg gcc aag tcc agg cag cgt cgc	597		
106	Lys Pro Glu Thr Gln Arg Arg Gly Trp Ala Lys Ser Arg Gln Arg Arg			
107	-50	-45	-40	-35
109	caa gtg tgg aag agg cgg gcg gaa gat ggg cag gga gac tcc ggt atc	645		
110	Gln Val Trp Lys Arg Arg Ala Glu Asp Gly Gln Gly Asp Ser Gly Ile			
111	-30	-25	-20	
113	tct tca cat ttc caa cct tgg ccc aag cat tcc ctt aaa cac agg gtc	693		
114	Ser Ser His Phe Gln Pro Trp Pro Lys His Ser Leu Lys His Arg Val			
115	-15	-10	-5	
117	aaa aag agt cca ccg gag gaa agc aac caa aat ggt gga gag ggc tcc	741		
118	Lys Lys Ser Pro Pro Glu Glu Ser Asn Gln Asn Gly Gly Glu Gly Ser			
119	-1 1 5 10			
121	tac cga gaa gca gag acc ttt aac tcc caa gta gga ctg ccc atc tta	789		
122	Tyr Arg Glu Ala Glu Thr Phe Asn Ser Gln Val Gly Leu Pro Ile Leu			
123	15 20 25 30			
125	tac ttc tct ggg agg cgg gag cgg ctg ctg ctg cgt cca gaa gtg ctg	837		
126	Tyr Phe Ser Gly Arg Arg Glu Arg Leu Leu Leu Arg Pro Glu Val Leu			
127	35 40 45			

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129	gct	gag	att	ccc	cgg	gag	gcg	ttc	aca	gtg	gaa	gcc	tgg	gtt	aaa	ccg	885
130	Ala	Glu	Ile	Pro	Arg	Glu	Ala	Phe	Thr	Val	Glu	Ala	Trp	Val	Lys	Pro	
131				50				55					60				
133	gag	gga	gga	cag	aac	aac	cca	gcc	atc	atc	gca	ggt	gtg	ttt	gat	aac	933
134	Glu	Gly	Gly	Gln	Asn	Asn	Pro	Ala	Ile	Ile	Ala	Gly	Val	Phe	Asp	Asn	
135			65					70					75				
137	tgc	tcc	cac	act	gtc	agt	gac	aaa	ggc	tgg	gcc	ctg	ggg	atc	cgc	tca	981
138	Cys	Ser	His	Thr	Val	Ser	Asp	Lys	Gly	Trp	Ala	Leu	Gly	Ile	Arg	Ser	
139		80					85					90					
141	ggg	aag	gac	aag	gga	aag	cgg	gat	gct	cgc	ttc	ttc	ttc	tcc	ctc	tgc	1029
142	Gly	Lys	Asp	Lys	Gly	Lys	Arg	Asp	Ala	Arg	Phe	Phe	Ser	Leu	Cys		
143	95					100					105				110		
145	acc	gac	cgc	gtg	aag	aaa	gcc	acc	atc	ttg	att	agc	cac	agt	cgc	tac	1077
146	Thr	Asp	Arg	Val	Lys	Lys	Ala	Thr	Ile	Leu	Ile	Ser	His	Ser	Arg	Tyr	
147				115						120					125		
149	caa	cca	ggc	aca	tgg	acc	cat	gtg	gca	gcc	act	tac	gat	gga	cgg	cac	1125
150	Gln	Pro	Gly	Thr	Trp	Thr	His	Val	Ala	Ala	Thr	Tyr	Asp	Gly	Arg	His	
151				130					135					140			
153	atg	gcc	ctg	tat	gtg	gat	ggc	act	cag	gtg	gct	agc	agt	cta	gac	cag	1173
154	Met	Ala	Leu	Tyr	Val	Asp	Gly	Thr	Gln	Val	Ala	Ser	Ser	Leu	Asp	Gln	
155			145				150					155					
157	tct	ggt	ccc	ctg	aac	agc	ccc	ttc	atg	gca	tct	tgc	cgc	tct	ttg	ctc	1221
158	Ser	Gly	Pro	Leu	Asn	Ser	Pro	Phe	Met	Ala	Ser	Cys	Arg	Ser	Leu	Leu	
159		160				165					170						
161	ctg	ggg	gga	gac	agc	tct	gag	gat	ggg	cac	tat	ttc	cgt	gga	cac	ctg	1269
162	Leu	Gly	Gly	Asp	Ser	Ser	Glu	Asp	Gly	His	Tyr	Phe	Arg	Gly	His	Leu	
163	175					180					185				190		
165	ggc	aca	ctg	gtt	ttc	tgg	tcg	acc	gcc	ctg	cca	caa	agc	cat	ttt	cag	1317
166	Gly	Thr	Leu	Val	Phe	Trp	Ser	Thr	Ala	Leu	Pro	Gln	Ser	His	Phe	Gln	
167				195						200					205		
169	cac	agt	tct	cag	cat	tca	agt	ggg	gag	gag	gaa	gcg	act	gac	ttg	gtc	1365
170	His	Ser	Ser	Gln	His	Ser	Ser	Gly	Glu	Glu	Glu	Ala	Thr	Asp	Leu	Val	
171				210					215					220			
173	ctg	aca	gcg	agc	ttt	gag	cct	gtg	aac	aca	gag	tgg	gtt	ccc	ttt	aga	1413
174	Leu	Thr	Ala	Ser	Phe	Glu	Pro	Val	Asn	Thr	Glu	Trp	Val	Pro	Phe	Arg	
175			225					230					235				
177	gat	gag	aag	tac	cca	cga	ctt	gag	gtt	ctc	cag	ggc	ttt	gag	cca	gag	1461
178	Asp	Glu	Lys	Tyr	Pro	Arg	Leu	Glu	Val	Leu	Gln	Gly	Phe	Glu	Pro	Glu	
179		240				245					250						
181	cct	gag	att	ctg	tcg	cct	ttg	cag	ccc	cca	ctc	tgt	ggg	caa	aca	gtc	1509
182	Pro	Glu	Ile	Leu	Ser	Pro	Leu	Gln	Pro	Pro	Leu	Cys	Gly	Gln	Thr	Val	
183	255					260					265				270		
185	tgt	gac	aat	gtg	gaa	ttg	atc	tcc	cag	tac	aat	gga	tac	tgg	ccc	ctt	1557
186	Cys	Asp	Asn	Val	Glu	Leu	Ile	Ser	Gln	Tyr	Asn	Gly	Tyr	Trp	Pro	Leu	
187				275						280				285			
189	cgg	gga	gag	aag	gtg	ata	cgc	tac	cag	gtg	gtg	aac	atc	tgt	gat	gat	1605
190	Arg	Gly	Glu	Lys	Val	Ile	Arg	Tyr	Gln	Val	Val	Asn	Ile	Cys	Asp	Asp	
191				290					295				300				
193	gag	ggc	cta	aac	ccc	att	gtg	agt	gag	gag	cag	att	cgt	ctg	cag	cac	1653

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194	Glu	Gly	Leu	Asn	Pro	Ile	Val	Ser	Glu	Glu	Gln	Ile	Arg	Leu	Gln	His	
195			305					310					315				
197	gag	gca	ctg	aat	gag	gcc	ttc	agc	cgc	tac	aac	atc	agc	tgg	cag	ctg	1701
198	Glu	Ala	Leu	Asn	Glu	Ala	Phe	Ser	Arg	Tyr	Asn	Ile	Ser	Trp	Gln	Leu	
199			320				325					330					
201	agc	gtc	cac	cag	gtc	cac	aat	tcc	acc	ctg	cga	cac	cgg	gtt	gtg	ctt	1749
202	Ser	Val	His	Gln	Val	His	Asn	Ser	Thr	Leu	Arg	His	Arg	Val	Val	Leu	
203	335						340					345				350	
205	gtg	aac	tgt	gag	ccc	agc	aag	att	ggc	aat	gac	cat	tgt	gac	ccc	gag	1797
206	Val	Asn	Cys	Glu	Pro	Ser	Lys	Ile	Gly	Asn	Asp	His	Cys	Asp	Pro	Glu	
207							355				360					365	
209	tgt	gag	cac	cca	ctc	aca	ggc	tat	gat	ggg	ggt	gac	tgc	cgc	ctg	cag	1845
210	Cys	Glu	His	Pro	Leu	Thr	Gly	Tyr	Asp	Gly	Gly	Asp	Cys	Arg	Leu	Gln	
211							370				375				380		
213	ggc	cgc	tgc	tac	tcc	tgg	aac	cgc	agg	gat	ggg	ctc	tgt	cac	gtg	gag	1893
214	Gly	Arg	Cys	Tyr	Ser	Trp	Asn	Arg	Arg	Asp	Gly	Leu	Cys	His	Val	Glu	
215							385					390				395	
217	tgt	aac	aac	atg	ctg	aac	gac	ttt	gac	gac	gga	gac	tgc	tgc	gac	ccc	1941
218	Cys	Asn	Asn	Met	Leu	Asn	Asp	Phe	Asp	Asp	Gly	Asp	Cys	Cys	Asp	Pro	
219							400					410					
221	cag	gtg	gct	gat	gtg	cgc	aag	acc	tgc	ttt	gac	cct	gac	tca	ccc	aag	1989
222	Gln	Val	Ala	Asp	Val	Arg	Lys	Thr	Cys	Phe	Asp	Pro	Asp	Ser	Pro	Lys	
223	415						420					425				430	
225	agg	gca	tac	atg	agt	gtg	aag	gag	ctg	aag	gag	gcc	ctg	cag	ctg	aac	2037
226	Arg	Ala	Tyr	Met	Ser	Val	Lys	Glu	Leu	Lys	Glu	Ala	Leu	Gln	Leu	Asn	
227							435					440				445	
229	agt	act	cac	ttc	ctc	aac	atc	tac	ttt	gcc	agc	tca	gtg	cgg	gaa	gac	2085
230	Ser	Thr	His	Phe	Leu	Asn	Ile	Tyr	Phe	Ala	Ser	Ser	Val	Arg	Glu	Asp	
231							450					455				460	
233	ctt	gca	ggt	gct	gcc	acc	tgg	cct	tgg	gac	aag	gac	gct	gtc	act	cac	2133
234	Leu	Ala	Gly	Ala	Ala	Thr	Trp	Pro	Trp	Asp	Lys	Asp	Ala	Val	Thr	His	
235							465					470				475	
237	ctg	ggt	ggc	att	gtc	ctc	agc	cca	gca	tat	tat	ggg	atg	cct	ggc	cac	2181
238	Leu	Gly	Gly	Ile	Val	Leu	Ser	Pro	Ala	Tyr	Tyr	Gly	Met	Pro	Gly	His	
239							480					485				490	
241	acc	gac	acc	atg	atc	cat	gaa	gtg	gga	cat	gtt	ctg	gga	ctc	tac	cat	2229
242	Thr	Asp	Thr	Met	Ile	His	Glu	Val	Gly	His	Val	Leu	Gly	Leu	Tyr	His	
243	495						500					505				510	
245	gtc	ttt	aaa	gga	gtc	agt	gaa	aga	gaa	tcc	tgc	aat	gac	ccc	tgc	aag	2277
246	Val	Phe	Lys	Gly	Val	Ser	Glu	Arg	Glu	Ser	Cys	Asn	Asp	Pro	Cys	Lys	
247							515					520				525	
249	gag	aca	gtg	cca	tcc	atg	gaa	acg	gga	gac	ctc	tgt	gcc	gac	acc	gcc	2325
250	Glu	Thr	Val	Pro	Ser	Met	Glu	Thr	Gly	Asp	Leu	Cys	Ala	Asp	Thr	Ala	
251							530					535				540	
253	ccc	act	ccc	aag	agt	gag	ctg	tgc	cgg	gaa	cca	gag	ccc	act	agt	gac	2373
254	Pro	Thr	Pro	Lys	Ser	Glu	Leu	Cys	Arg	Glu	Pro	Glu	Pro	Thr	Ser	Asp	
255							545					550				555	
257	acc	tgt	ggc	ttc	act	cgc	ttc	cca	ggg	gct	ccg	ttc	acc	aac	tac	atg	2421
258	Thr	Cys	Gly	Phe	Thr	Arg	Phe	Pro	Gly	Ala	Pro	Phe	Thr	Asn	Tyr	Met	

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259	560	565	570	
261	agc tac acg gat gat aac tgc act gac aac ttc act cct aac caa gtg	2469		
262	Ser Tyr Thr Asp Asp Asn Cys Thr Asp Asn Phe Thr Pro Asn Gln Val			
263	575	580	585	590
265	gcc cga atg cat tgc tat ttg gac cta gtc tat cag cag tgg act gaa	2517		
266	Ala Arg Met His Cys Tyr Leu Asp Leu Val Tyr Gln Gln Trp Thr Glu			
267		595	600	605
269	agc aga aag ccc acc ccc atc ccc att cca cct atg gtc atc gga cag	2565		
270	Ser Arg Lys Pro Thr Pro Ile Pro Ile Pro Pro Met Val Ile Gly Gln			
271		610	615	620
273	acc aac aag tcc ctc act atc cac tgg ctg cct cct att agt gga gtt	2613		
274	Thr Asn Lys Ser Leu Thr Ile His Trp Leu Pro Pro Ile Ser Gly Val			
275		625	630	635
277	gta tat gac agg gcc tca ggc agc ttg tgt ggc gct tgc act gaa gat	2661		
278	Val Tyr Asp Arg Ala Ser Gly Ser Leu Cys Gly Ala Cys Thr Glu Asp			
279		640	645	650
281	ggg acc ttt cgt cag tat gtg cac aca gct tcc tcc cgg cgg gtg tgt	2709		
282	Gly Thr Phe Arg Gln Tyr Val His Thr Ala Ser Ser Arg Arg Val Cys			
283		655	660	665
285	gac tcc tca ggt tat tgg acc cca gag gag gct gtg ggg cct cct gat	2757		
286	Asp Ser Ser Gly Tyr Trp Thr Pro Glu Glu Ala Val Gly Pro Pro Asp			
287		675	680	685
289	gtg gat cag ccc tgc gag cca agc tta cag gcc tgg agc cct gag gtc	2805		
290	Val Asp Gln Pro Cys Glu Pro Ser Leu Gln Ala Trp Ser Pro Glu Val			
291		690	695	700
293	cac ctg tac cac atg aac atg acg gtc ccc tgc ccc aca gaa ggc tgt	2853		
294	His Leu Tyr His Met Asn Met Thr Val Pro Cys Pro Thr Glu Gly Cys			
295		705	710	715
297	agc ttg gag ctg ctc ttc caa cac ccg gtc caa gcc gac acc ctc acc	2901		
298	Ser Leu Glu Leu Leu Phe Gln His Pro Val Gln Ala Asp Thr Leu Thr			
299		720	725	730
301	ctg tgg gtc act tcc ttc ttc atg gag tcc tcg cag gtc ctc ttt gac	2949		
302	Leu Trp Val Thr Ser Phe Phe Met Glu Ser Ser Gln Val Leu Phe Asp			
303		735	740	745
305	aca gag atc ttg ctg gaa aac aag gag tca gtg cac ctg ggc ccc tta	2997		
306	Thr Glu Ile Leu Leu Glu Asn Lys Glu Ser Val His Leu Gly Pro Leu			
307		755	760	765
309	gac act ttc tgt gac atc cca ctc acc atc aaa ctg cac gtg gat ggg	3045		
310	Asp Thr Phe Cys Asp Ile Pro Leu Thr Ile Lys Leu His Val Asp Gly			
311		770	775	780
313	aag gtg tcg ggg gtg aaa gtc tac acc ttt gat gag agg ata gag att	3093		
314	Lys Val Ser Gly Val Lys Val Tyr Thr Phe Asp Glu Arg Ile Glu Ile			
315		785	790	795
317	gat gca gca ctc ctg act tct cag ccc cac agt ccc ttg tgc tct ggc	3141		
318	Asp Ala Ala Leu Leu Thr Ser Gln Pro His Ser Pro Leu Cys Ser Gly			
319		800	805	810
321	tgc agg cct gtg agg tac cag gtt ctc cgc gat ccc cca ttt gcc agt	3189		
322	Cys Arg Pro Val Arg Tyr Gln Val Leu Arg Asp Pro Pro Phe Ala Ser			
323		815	820	825
				830

RAW SEQUENCE LISTING ERROR SUMMARY  
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Please Note:

Use of n and/or Xaa have been detected in the Sequence Listing. Please review the Sequence Listing to ensure that a corresponding explanation is presented in the <220> to <223> fields of each sequence which presents at least one n or Xaa.

Seq#:3; Xaa Pos. 3,4,6,7,9,10  
Seq#:24; Xaa Pos. 3  
Seq#:26; Xaa Pos. 3,4,6,7,9,10

Invalid <213> Response:

Use of "Artificial" only as "<213> Organism" response is incomplete,  
per 1.823(b) of New Sequence Rules. Valid response is Artificial Sequence.

Seq#:26

**VERIFICATION SUMMARY**

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L:1132 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:3 after pos.:0  
L:1402 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:24 after pos.:0  
L:1859 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:26 after pos.:0